

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=1; day=8; hr=10; min=22; sec=40; ms=875;]

=====

Reviewer Comments:

Glu Leu Leu Asn Ser Met Asn. Ile Ser Gln Pro Thr Val Val Phe Val
115 120 125

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
370 375 380

Please delete invalid alpha numeric character appearing beside amino acid coding Asn at position 119 in the above sequence id# 39. Please also correct invalid amino acid numbering appearing above at position 375 in the sequence, please check the remaining sequences for similar errors.

Phe Lue Arg Ser Lue Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val
275 280 285

Please also correct invalid amino acid coding Lue appearing at position 274 and 277 in the above sample of sequence id# 41.

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
65 70 75 80

Pro Ile Phe Gly ASn Gln Ile Xaa Pro Asp Thr Ala Ile Leu Ser Val
225 230 235 240

Per the above sample of sequence id# 42, please correct invalid amino acid numbering at position 75 in the sequence. Please also correct invalid amino acid coding ASn at position 229 in the sequence.

Application No: 09763824

Version No: 5.0

Input Set:**Output Set:**

Started: 2008-12-24 10:25:15.658
Finished: 2008-12-24 10:25:19.413
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 755 ms
Total Warnings: 36
Total Errors: 8
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2008-12-24 10:25:15.658
Finished: 2008-12-24 10:25:19.413
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 755 ms
Total Warnings: 36
Total Errors: 8
No. of SeqIDs Defined: 42
Actual SeqID Count: 42

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 330	Invalid protein , found in SEQID(39) POS (119) Invalid
E 323	Invalid/missing amino acid numbering SEQID (39)at Protein (375)
E 323	Invalid/missing amino acid numbering SEQID (39) POS (376)
E 330	Invalid protein , found in SEQID(41) POS (274) Invalid Protein:Lue
E 330	Invalid protein , found in SEQID(41) POS (277) Invalid Protein:Lue
E 323	Invalid/missing amino acid numbering SEQID (42) POS (73)
E 323	Invalid/missing amino acid numbering SEQID (42)at Protein (75)
E 330	Invalid protein , found in SEQID(42) POS (229) Invalid Protein:ASn

<110> SQUIRRELL, DAVID J.
MURPHY, MELANIE J.
PRICE, RACHEL L.
LOWE, CHRISTOPHER R.
WHITE, PETER J.
TISI, LAURENCE C.
MURRAY, JAMES A. H.

<120> NOVEL ENZYME

<130> 1498-119

<140> 09763824
<141> 2001-02-27

<150> PCT/GB99/03538
<151> 1999-10-26

<150> GB 9823468.5
<151> 1998-10-28

<160> 42

<170> PatentIn Ver. 2.1

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<220>

<223> Description of Artificial Sequence: Primer

<400> 1
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23

<210> 2

<211> 23

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 2

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23

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<211> 51

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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cgaacacttc ttcatcggtt accgccttaa gttttttaatt aaatacaaaag g 51

<210> 4
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<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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ctttttgtatt taattaaaga cttaaaggcgg tcaactatga agaagtgttc g 51

<210> 5
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 5
gaaaaggcccg gcaaccggcct atccctctaga gg 32

<210> 6
<211> 32
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 6
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<210> 7
<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 7
ccataaaattt accggatcttc tggacttgcg tggagg 36

<210> 8
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 8
gtgtggaaatt gtgagcggg 18

<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 9
qagatacggcc gggtttcctg g 21

<210> 10
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<220>
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ccaggaaaccg cggcgatact c 21

<210> 11
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 11
ccctattttc attcctggcc aaaaagcactc 30

<210> 12
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<213> Artificial Sequence

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<212> DNA
<213> Artificial Sequence

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ccgcatacggat ctctctgcgt cagat 27

<210> 14
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gaatctgacg cagagagtc tatgcgg 27

<210> 15
<211> 30
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 15
gttgacgcgt tggatccctt aattttatcc 30

<210> 16
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 16
gtatagattt gaaaaagagc tg 22

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 17
cagcttttt tcaaatctat ac 22

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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ggttacatac tggagacata gc 22

<210> 19

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<211> 22
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 19
gtatgttctt cagtatgtat cc 22

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<213> Artificial Sequence

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gcagggttgcgc cctgtgtacgc c 21

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gttgttcaag ggcgcacgtt c 21

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<213> Artificial Sequence

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caaatccatcc cgggtactgc gatttttag 29

<210> 23
<211> 29
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<210> 24

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<211> 27
<212> DNA
<213> Artificial Sequence

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<400> 24
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<210> 25
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<210> 26
<211> 22
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ctgattacac ccaaggggga tg 22

<210> 27
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<212> DNA
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<223> Description of Artificial Sequence: Primer

<400> 27
catccccctt ggggttaatc ag 22

<210> 28
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<212> DNA
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<220>
<221> modified_base
<222> (15)..(17)
<223> a, g, c or t

<400> 28

cccttcggca tagannngcc tgcgtcagt 29
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<220>
<221> modified_base
<222> (13)..(15)
<223> a, g, c or t

<400> 29
actgacgcag gcnntctat gggaaagg 29

<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 30
gcaatcaaat cgctccggat actgc 25

<210> 31
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
gcaatccatcg gacggatttg attgc 25

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
ccatccatca aaggttttgg 20

<210> 33
<211> 20
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

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ccaaaaacctt gatggaaatgg

20

<210> 34
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 34
aaacacggggac ccatatggaa gacgc

25

<210> 35
<211> 36
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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atattaactcg aggaatttcg tcatacgctga atacag

35

<210> 36
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 36
cccttatttc attcttggcc aaaaacactg

30

<210> 37
<211> 550
<212> PRT
<213> Photinus pyralis

<400> 37
Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro
1 5 10 15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg
20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
35 40 45

Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
100 105 110

Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val Val Phe Val
115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
130 135 140

Ile Ile Gln Lys Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
145 150 155 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
165 170 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
180 185 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
195 200 205

Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp
210 215 220

Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val
225 230 235 240

Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu
245 250 255

Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu
260 265 270

Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val
275 280 285

Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr
290 295 300

Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser
305 310 315 320

Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile
325 330 335

Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr
340 345 350

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe
355 360 365

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
405 410 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
435 440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile
450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu
465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu
500 505 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly
515 520 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys
530 535 540

Gly Gly Lys Ser Lys Leu
545 550

<210> 38
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<213> Photinus pyralis

<220>
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1 5 10 15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg
20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
35 40 45

Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala

50

55

60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
 65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
 85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
 100 105 110

Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val Val Phe Val
 115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
 130 135 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
 145 150 155 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe
 165 170 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile
 180 185 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val
 195 200 205

Ala Leu Pro His Arg Xaa Ala Cys Val Arg Phe Ser His Ala Arg Asp
 210 215 220

Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val
 225 230 235 240

Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu
 245 250 255

Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu
 260 265 270

Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val
 275 280 285

Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr
 290 295 300

Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser
 305 310 315 320

Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile
 325 330 335

Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr
 340 345 350

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe

355

360

365

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val
 370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly
 385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly
 405 410 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe
 420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln
 435 440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile
 450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu
 465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys
 485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu
 500 505 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly
 515 520 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys
 530 535 540

Gly Gly Lys Ser Lys Leu
 545 550

<210> 39
 <211> 550
 <212> PRT
 <213> Photinus pyralis

<220>
 <221> VARIANT
 <222> (214)
 <223> Xaa-Cys, Ala or Asn

<400> 39
 Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro
 1 5 10 15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg
 20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu
 35 40 45

Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala
50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val
65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu
85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg
100 105 110

Glu Leu Leu Asn Ser Met Asn. Ile Ser Gln Pro Thr Val Val Phe Val
115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro
130 135 140

Ile Ile Gln Lys Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly
1